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PATENT
Attorney Docket No.: 02307E-114910US
Client Ref. No.: 2001-124-2

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

On April 28, 2005

TOWNSEND and TOWNSEND and CREW LLP

By: Patricia Anders

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Zuker et al.

Application No.: 10/026,188

Filed: December 21, 2001

For: ASSAYS FOR TASTE RECEPTOR
CELL SPECIFIC ION CHANNEL

Customer No.: 20350

Confirmation No. 9521

Examiner: Michael T. Brannock

Technology Center/Art Unit: 1646

Declaration of Charles S. Zuker and Yifeng
Zhang pursuant to 37 C. F. R. §1.131

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

We, Charles S. Zuker and Yifeng Zhang, being duly warned that willful false statements and the like are punishable by fine or imprisonment or both, under 18 U.S.C. §1001, and may jeopardize the validity of the patent application or any patent issuing thereon, state and declare as follows:

1. All statements herein made of our own knowledge are true and statements made on information or belief are believed to be true. Exhibits I-V are attached hereto and incorporated herein by reference.

2. At the time this invention was first conceived, we were employees of Howard Hughes Medical Institute and the University of California, located in San Diego, California. All activities described in this Declaration took place in the United States of America.

3. In accordance with 37 C.F.R. §1.131, we state that we completed the claimed invention in the United States prior to April 17, 2000, the filing date of USSN 60/197,491, to which published U.S. Patent Application US 2002/0037515 claims priority.

4. Attached to this Declaration are:

Exhibit I, pages of a printout of a sequence file containing the polynucleotide sequence of 930 clones obtained from a subtracted cDNA library prepared from rat circumvallate cells, following the experimental procedure described in Example I of the application. The pages of Exhibit I indicate the date of last modification to contiguous sequence ("contig") No. 068-3 157 501 and the polynucleotide sequence of clone 501, one of the three clones that make up this contig;

Exhibit II, pages of laboratory notebook indicating that a Blast search was performed for known polynucleotide sequences matching each one of the 930 clones, including clone 501;

Exhibit III, results of sequence alignment between the mouse Trpm5 (also known as Mtr1 and Ltrpc5) and clone 501, which indicate a high degree of homology;

Exhibit IV, polynucleotide sequences of the mouse Trpm5 (GenBank No. NM_020277, derived from GenBank No. AJ271092, see page 2 of printout for NM_020277) and human Mtr1 (GenBank No. AF177473), which indicate that these sequences were publicly accessible by January 14, 2000 (see page 1 of printout for AJ271092) and August 13, 1999 (see page 1 of printout for AF177473), respectively. Exhibit IV further includes results of a sequence alignment between the amino acid sequences encoded by mouse Trpm5 gene and human Mtr1 gene; and

Exhibit V, results of an *in situ* hybridization experiment indicating the taste cell-specific expression of the gene from which clone 501 is derived, using a nucleic acid probe specific for clone 501, which was also referred to as 501-PCR46. Some dates in the Exhibits have been redacted. All redacted dates in the Exhibits are prior to April 17, 2000.

5. Conception of the present invention as well as its reduction to practice are evidenced by Exhibits I-IV. The first page of Exhibit I shows that contig No. 068-3 157 501 consists of three clones: 3, 157, and 501, the longest of which is clone 501. The second page shows the polynucleotide sequence of clone 501. The third page establishes the time of last modification made to contig No. 068-3 157 501 and therefore establishes the time when the sequence of clone 501 was determined. Upon determination of the polynucleotide sequence of clone 501, a Blast search was conducted to identify known polynucleotide sequence(s) with high level of sequence homology with clone 501. This is evidenced by Exhibit II.

6. The identification of the mouse Trpm5 gene through this sequence homology-based search is evidenced by Exhibit III, which demonstrates that the mouse Trpm5 and clone 501 are highly homologous. Therefore, one of skill in the art would consider the rat gene from which clone 501 is derived to be the ortholog of mouse Trpm5. Although this particular sequence alignment shown in Exhibit III was performed at the present time, the same result would have been (and was indeed) obtained at the time the initial Blast search was performed. This is because, as evidenced by Exhibit IV, the polynucleotide sequence of mouse Trpm5 was publicly accessible well before April 17, 2000. Furthermore, Exhibit IV establishes that human Mtr1 and mouse Trpm5 have a greater than 84% identity in amino acid sequence. Based on this high level of sequence homology, one of skill in the art would recognize human Mtr1 as the ortholog of mouse Trpm5. In addition, Exhibit IV also demonstrates that the polynucleotide sequence of human Mtr1 gene was publicly available well before April 17, 2000. Thus, a Blast search based on the sequence of clone 501 by the present inventors at the time indicated by Exhibit II necessarily led to the identification of both the human and mouse versions of the Mtr1 gene. Subsequently, *in situ* hybridization was performed to confirm the taste cell-specific expression of the rat version of this gene, shown in Exhibit V. It is therefore established that,

Appl. No. 10/026,188
Declaration under 37 C.F.R. §1.131
Reply to Office Action of November 30, 2004


PATENT

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.

7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

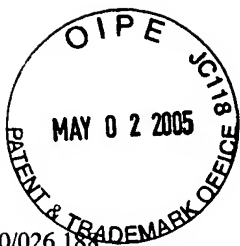
Dated: 4/13/05

By: 
Charles S. Zuker, Ph.D.

Dated: _____

By: _____
Yifeng Zhang, Ph.D.

Attachments (Exhibits I-V)
60427031 V1



Appl. No. 10/026,188
Declaration under 37 C.F.R. §1.131
Reply to Office Action of November 30, 2004

PATENT

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.


7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

Dated: _____

By: _____
Charles S. Zuker, Ph.D.

Dated: 4/20/05

By: 
Yifeng Zhang, Ph.D.

Attachments (Exhibits I-V)
60427031 V1

Rat Sub Seq 12/99 copy
Sequencher™ "Rat Sub Seq 12/99 copy"

Name	Size	Kind	Label	Last Modified
042 GS	205 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:58:
043 GS	392 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
044 86	700 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:44:
045	284 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:33:
046 GS	486 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
047	192 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
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049 262-5 GS	408 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:07:
050 120 659	571 BPs	Contig of 3	-	Thu, Feb 3, 2000 8:14:
051 854	350 BPs	Contig of 2	-	Thu, Feb 3, 2000 8:14:
052	603 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
053 3'	105 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:32:
053-5 487-5 GS	309 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:49:
053mid 303	268 BPs	Contig of 2	-	Wed, Jan 19, 2000 6:19:
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056	87 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
057 76 178 464 515-...	252 BPs	Contig of 7	-	Thu, Feb 3, 2000 11:11:
059	330 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
060 895-3 ok	307 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:11:
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064	609 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
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070 493-5 648-5	351 BPs	Contig of 3	-	Thu, Feb 3, 2000 11:11:
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073 815-3	544 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:49:
074 GS	439 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:20:
075 510 229 831 88...	322 BPs	Contig of 6	-	Wed, Jan 19, 2000 6:19:
078 GS	587 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:22:

Differential Screening + Sequencing

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Hybond N+ lifts

autoclave 5'

rinse to get rid of the debris

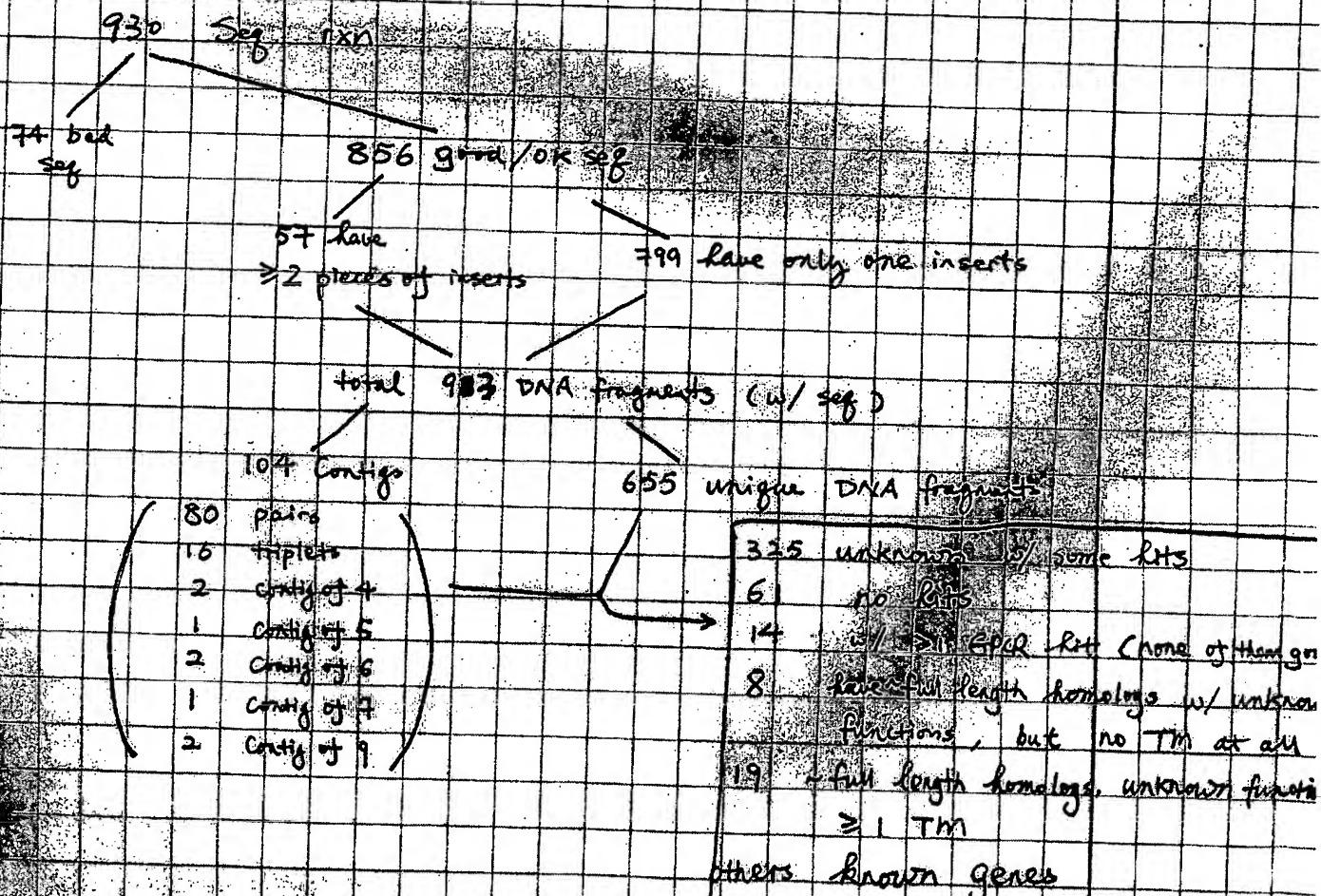
Hyb: w/ sub - (reverse subtracted) as probe

Pick white
Unlighted-up colonies (930)

Miniprep (Clontech 96)

Sequencing (5µl of each DNA sample)

Report



(Continued)

II. SF-615 Ena Assay

Not Working !!

Cell lines tried

① Peak Rapid Rb Gx15

② Peak Rapid



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

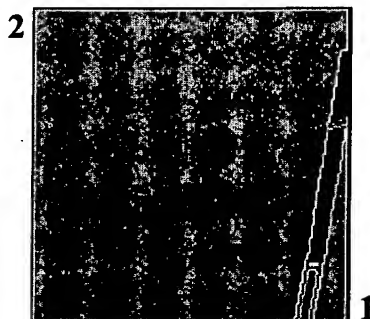
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: [Filter](#) [Align](#)

Sequence	gi	Mus musculus transient receptor potential cation channel,	Length 4032	(1 ..
1	12383053	subfamily M, member 5 (Trpm5), mRNA	4032)	
Sequence	lcl 501	contig	Length 627	(1 ..
2			627)	



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 371 bits (193), Expect = 7e-99
Identities = 349/414 (84%), Gaps = 9/414 (2%)
Strand = Plus / Plus

|||||

Query: 3583 ccttgctacagatcacttcttggacatcccttcctaagagaatgaaactcatgtccttgg 3642
||||| ||||| || ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 127 ccttgccgcagaccatgtcttggacacctcttcctatgaaaatgagactcatgtccttgg 186

Query: 3643 catctattcgggagcctcagaagtatcctctccagcagggcaagatTTTTcatgtccac 3702
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 187 catctatctgggagcccaggcgt--cctctccagcaggggaagtttctcatgtcctac 244

Query: 3703 -taaagctttcactggccttggactggacagctggatctggccaagtcctacataggacac 3761
|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 245 ctaaaactttcaccagctaagactggacagctggaactggccaagtcccacatgggatac 304

Query: 3762 catctgcctggatggggctatttaggtctaaccctgtcttaccctgagttcctaagaag 3821
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Query: 3939 cattatctgtctgatcattctggca-gaaaccccaagatattgctcaaggggtac 3991
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Score = 160 bits (83), Expect = 3e-35
Identities = 114/127 (89%), Gaps = 1/127 (0%)
Strand = Plus / Plus



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|||||
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| |||||
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Query: 3562 cccaaga 3568
||| |||
Sbjct: 120 cccgaga 126




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Lambda	K	H
1.33	0.621	1.12

Gapped Lambda	K	H
1.33	0.621	1.12

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Gap Penalties: Existence: 5, Extension: 2

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Number of Hits to DB: 69
Number of extensions: 11
Number of successful extensions: 8
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
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Length adjustment: 27
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Effective search space: 53559591607125
Effective search space used: 53559591607125
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

Range: from to
☐ Reverse complemented strand
 Features: ☐ SNP ☐ CDD
 ☒ MGC ☐ HPRD

☐ 1: [NM_020277](#). Reports *Mus musculus* tran...[gi:12383053]

[Links](#)

LOCUS NM_020277 4032 bp mRNA linear ROD 26-OCT-2004
 DEFINITION *Mus musculus* transient receptor potential cation channel, subfamily M, member 5 (Trpm5), mRNA.
 ACCESSION NM_020277
 VERSION NM_020277.1 GI:12383053
 KEYWORDS
 SOURCE *Mus musculus* (house mouse)
 ORGANISM *Mus musculus*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 4032)
 AUTHORS Liu,D. and Liman,E.R.
 TITLE Intracellular Ca²⁺ and the phospholipid PIP₂ regulate the taste transduction ion channel TRPM5
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (25), 15160-15165 (2003)
 PUBMED 14657398
 REMARK GeneRIF: regulation of TRPM5 by Ca²⁺ mediates sensory activation in the taste system
 REFERENCE 2 (bases 1 to 4032)
 AUTHORS Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
 TITLE TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel
 JOURNAL Curr. Biol. 13 (13), 1153-1158 (2003)
 PUBMED 12842017
 REFERENCE 3 (bases 1 to 4032)
 AUTHORS Perez,C.A., Huang,L., Rong,M., Kozak,J.A., Preuss,A.K., Zhang,H., Max,M. and Margolskee,R.F.
 TITLE A transient receptor potential channel expressed in taste receptor cells
 JOURNAL Nat. Neurosci. 5 (11), 1169-1176 (2002)
 PUBMED 12368808
 REMARK GeneRIF: functions as a cationic channel that is gated when internal calcium stores are depleted and may be responsible for capacitative calcium entry in taste receptor cells that respond to bitter and/or sweet compounds.
 REFERENCE 4 (bases 1 to 4032)
 AUTHORS Paulsen,M., El-Maarri,O., Engemann,S., Stroedicke,M., Franck,O., Davies,K., Reinhardt,R., Reik,W. and Walter,J.
 TITLE Sequence conservation and variability of imprinting in the Beckwith-Wiedemann syndrome gene cluster in human and mouse
 JOURNAL Hum. Mol. Genet. 9 (12), 1829-1841 (2000)
 PUBMED 10915772
 REFERENCE 5 (bases 1 to 4032)
 AUTHORS Enklaar,T., Esswein,M., Oswald,M., Hilbert,K., Winterpacht,A., Higgins,M., Zabel,B. and Prawitt,D.
 TITLE Mtr1, a novel biallelically expressed gene in the center of the mouse distal chromosome 7 imprinting cluster, is a member of the Trp gene family

JOURNAL Genomics 67 (2), 179-187 (2000)
PUBMED [10903843](#)
REFERENCE 6 (bases 1 to 4032)
AUTHORS Yatsuki,H., Watanabe,H., Hattori,M., Joh,K., Soejima,H., Komoda,H.,
Xin,Z., Zhu,X., Higashimoto,K., Nishimura,M., Kuratomi,S.,
Sasaki,H., Sakaki,Y. and Mukai,T.
TITLE Sequence-based structural features between Kvlqt1 and Tapal on
mouse chromosome 7F4/F5 corresponding to the Beckwith-Wiedemann
syndrome region on human 11p15.5: long-stretches of unusually well
conserved intronic sequences of kvlqt1 between mouse and human
JOURNAL DNA Res. 7 (3), 195-206 (2000)
PUBMED [10907850](#)
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
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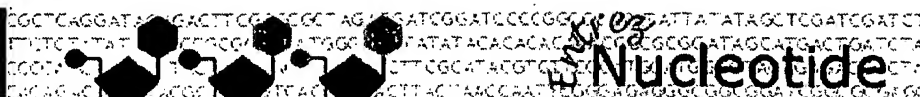
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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD
☒ MGC ☐ HPRD

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 Davies,K., Reinhardt,R., Reik,W. and Walter,J.
 TITLE Sequence conservation and variability of imprinting in the
 beckwith-wiedemann syndrome gene cluster in human and mouse
 JOURNAL Hum. Mol. Genet. 9 (12), 1829-1841 (2000)
 MEDLINE 20377495
 REFERENCE 2 (bases 1 to 4691)
 AUTHORS Stroedicke,M.
 TITLE Direct Submission
 JOURNAL Submitted (14-JAN-2000) Stroedicke M., T.A.Trautner,
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2341	ctggtgctgg	aggaaatccg	gcagggcttc	ttcacagacg	aggacacaca	cctggtgaag
2401	aagttcacac	tgtatgtggg	ggacaactgg	aacaagtgtg	acatggtggc	catcttctct
2461	ttcatcgtgg	gtgtcacctg	caggatgctg	ccgtcggcgt	ttgaggctgg	ccgcacggct
2521	ctcgccatgg	acttcatggt	gttcacgctg	cggctgatcc	atatctttgc	catacacaag
2581	cagctggggc	ccaagatcat	cgtggttagg	cgcatgatga	aggacgtctt	cttcttcctc
2641	ttctttctga	gcgtgtggct	cgtggcctac	ggtgtcacca	cccaggcgct	gctgcacccc
2701	catgacggcc	gcctggagtg	gatcttccgc	cgggtgctct	accggcccta	cctgcagatc
2761	ttcgccaga	tcccactgga	cgagattgat	gaagcccgtg	tgaactgctc	caccacccca
2821	ctgctgctgg	aggactcacc	atcctgcccc	agcctctatg	ccaactggct	ggtcatcctc

```
2881 ctgctgggtca ccttcctggt ggtcaccaat gtgctgctca tgaacctgct catcgccatg
2941 ttcagctaca cgttccaggt ggtgcagggc aacgcagaca tgttctggaa gttccagcgc
3001 tacaacctga ttgtggagta ccacgagcgc cccgccctgg ccccgccctt catcctgctc
3061 agccacctga gcctgacgct ccgccgggtc ttcaagaagg aggctgagca caagcgggag
3121 cacctggaga gagacctgcc agacccctg gaccagaagg tcgtcacctg ggagacagtc
3181 cagaaggaga acttcctgag caagatggag aagcggagga gggacagcga gggggagggtg
3241 ctgcggaataa ccgcccacag agtggacttc attgccaagt acctcggggg gctgagagag
3301 caagaaaagc gcatcaagtg tctggagtca cagatcaact actgctcggg gctcgtgtcc
3361 tccgtggctg acgtgctggc ccaggggtgg gcccccggg gctctcagca ctgtggcgag
3421 ggaagccagc tgggtggctgc tgaccacaga ggtgggttag atggctggga acaaccggg
3481 gctggccagc ctccctcgga cacatgagct gcttggcctg ccacgtgtgg ggccacctct
3541 cttcagttgg ccacctgca cgttgtgcac tgacctttgc cgacctccag cggaaacccc
3601 cagggggcac cagcccccca gcagacaatg gccctcctgg tgcctacca cagacctca
3661 cccaaaggaa ccgctccttg tccctcctgg cctccccgga ggcacagcag tgtcatgggg
3721 ctgtctcccc tgacaggcac aactccccgg gcagaaaacg tgccccaccg catccctacc
3781 tggaaactga ccagcctgca ctgtggaaaa gctggccctg tggcgtgacg ggggagcacc
3841 cccatccaga ctgcgaagct gctctgggtc tgcaccacc cctgccctga cttgtgttgc
3901 ctgacaagag act
```

//

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Feb 9 2005 14:31:10

Align two sequences

Tue Mar 1 21:52:38 "GMT 2005

```
/usr/tmp/seq1.73316.sca : 1158 aa
>Mouse MTR1, 1158 bases, 31D4F27D checksum.      1158 aa vs.
>Human MTR1, 1165 bases, C1D16397 checksum.      1165 aa
scoring matrix: , gap penalties: -12/-2
84.1% identity;      Global alignment score: 6543
```

```
      10      20      30      40      50      60
/usr/t MQTTQSSCPGSPPDTEGWEPILCRGEINFGGSGKKRGKFKVKVPSSVAPSVLFELLTEW
      :: ...  :::: :::: : : ::::::::::::::::::::::::::::::::::::::
Human  MQDVQGP RP GSPGDAEDRRELGLHRGEVNF GGSGKKRGKFKVRVPSGVAPSVLFDLLAEW
      10      20      30      40      50      60

      70      80      90     100     110     120
/usr/t HLPAPNLVSVSLVGEE RPLAMKSWLRDVL RKG L VKAAQSTGAWILTSALHVGLARHVGQAV
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Human  HLPAPNLVSVSLVGEE QPFAMKSWLRDVL RKG L VKAAQSTGAWILTSALRVGLARHVGQAV
      70      80      90     100     110     120

      130     140     150     160     170     180
/usr/t RDHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDTPIHYPADENIQGPLCPLDS
      :::::::::::::::::::::: ::::: . . . : :::: : . . . : :::: :
Human  RDHSLASTSTKVRVAVGMASLGRVLHRRILE--EAQEDFPVHYPEDDGGSGGPLCSLDS
      130     140     150     160     170

      190     200     210     220     230     240
/usr/t NLSHFILVESGALGSGNDGLTELQLSLEKHISQORTGYGGTSCIQIPVLCLLVNGDPNTL
      :::::::::: : :: ::::::::::::::::::::::::::::::::::::::::::::::
Human  NLSHFILVEPGPPGKG-DGLTELRLRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTL
      180     190     200     210     220     230

      250     260     270     280     290     300
/usr/t ERISRAVEQAAPWLILAGSGGIADVLAALVSQPHLLVPQVAEKQFREKFPSECF SWEAIV
      :::::::::::::::::::::::::::::::::::::::::::::::::::::: : ::
Human  ERISRAVEQAAPWLILVSGSGGIADVLAALVNQPHLLVPKVAEKQFKEKFP SKHFSWEDIV
      240     250     260     270     280     290

      310     320     330     340     350     360
/usr/t HWTELLQNIAAHPHLLTVYDFEQEGSELDLTVILKALVKACKSHSQEAQDYLDLKLAVA
      :::::::::: : ::::::::::::::::::::::::::::::::::::::::::::::
Human  RWTKLLQNITSHQHLLTVYDFEQEGSELDLTVILKALVKACKSHSQEPQDYLDLKLAVA
      300     310     320     330     340     350

      370     380     390     400     410     420
/usr/t WDRVDIAKSEIFNGDVEWKSCDLEEVMTDALVSNKPDFVRLFVDSGADMAEFLTYGRLQQ
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Human  WDRVDIAKSEIFNGDVEWKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLQE
      360     370     380     390     400     410

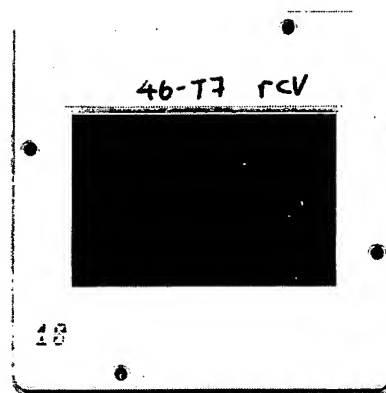
      430     440     450     460     470     480
/usr/t LYHSVSPKSLLFELLQRKHEEGRLTLAGLGAQQARELP IGLPAFSLHEVSRVLKD FLHDA
      ::::: : :::::::::::::::::::::::::::::: : : ::::::::::::::::::::::
Human  LYRSVSRKSLLFDLLQRKQEEARLTLAGLGTQQAREPPAGPPAFSLHEVSRVLKD FLQDA
      420     430     440     450     460     470
```



```
Human  LRKTAHRVDFIAKYLGGLREQEKRIKCLESQINYCSVLVSSVADVLAQGGGPRSSQHCGE
      1080      1090      1100      1110      1120      1130

      1140      1150
/usr/t RSQPASARDREYLE-----SGLPPSDT
      :: ... : .. .. : ::::
Human  GSQLVAADHRGGLDGWEQPGAGQPPSDT
      1140      1150      1160
```

Elapsed time: 0:00:00





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